

SEQUENCE LISTING

RECEIVED

MAY 2 1 2002

TECH CENTER 1600/2900

```
<110> willson, Tracy
       Nicola, Nicos A.
       Hilton, Douglas J.
Metcalf, Donald
       Zhang, Jian G.
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<120> NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES **ENCODING SAME**

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<130> Davies cc
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<140> 09/051,843

<141> 1998-06-29

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<170> PatentIn Ver. 2.0

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Go

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	att Ile	tta Leu	gag Glu 275	gtt Val	gaa Glu	gag Glu	gac Asp	aaa Lys 280	tgc Cys	cag Gln	aat Asn	tcc Ser	gaa Glu 285	tct Ser	gat Asp	aga Arg	924
	aac Asn	atg Met 290	gag Glu	ggt Gly	aca Thr	agt Ser	tgt Cys 295	ttc Phe	caa Gln	ctc Leu	cct Pro	ggt Gly 300	gtt val	ctt Leu	gcc Ala	gac Asp	972
	gct Ala 305	gtc Val	tac Tyr	aca Thr	gtc Val	aga Arg 310	gta Val	aga Arg	gtc Val	aaa Lys	aca Thr 315	aac Asn	aag Lys	tta Leu	tgc Cys	ttt Phe 320	1020
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	ctg Leu	ata Ile	gaa Glu	aac Asn 420	ctg Leu	aag Lys	aaa Lys	gca Ala	gct Ala 425	cct Pro	tgat	gggg	gag a	aagt	gatti	c	1358
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Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
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Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
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Ala Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
20 25 30
                                                                                  156
cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata
Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
35 40
                                                                                  204
                                                                Thr Val Ile
tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg
Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
                                                                                  252
      50
tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa
Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
65 70 75
                                                                                   300
act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa
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Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg
Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
                                                                                   396
               100
                                        105
gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg
                                                                                   444
Val Ğlu Lys Cys Ile Ser Pro Pro Ğlu Ğly Asp Pro Ğlü Ser Ala Val
act gag ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct
                                                                                   492
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tat Tyr	tgg Trp	cac His	aga Arg	agc Ser 165	ctg Leu	gaa Glu	aaa Lys	att Ile	cat His 170	caa Gln	tgt Cys	gaa Glu	aac Asn	atc Ile 175	ttt Phe	588
aga Arg	gaa Glu	ggc Gly	caa Gln 180	tac Tyr	ttt Phe	ggt Gly	tgt Cys	tcc Ser 185	ttt Phe	gat Asp	ctg Leu	acc Thr	aaa Lys 190	gtg Val	aag Lys	636
gat Asp	tcc Ser	agt Ser 195	ttt Phe	gaa Glu	caa Gln	cac His	agt Ser 200	gtc val	caa Gln	ata Ile	atg Met	gtc Val 205	aag Lys	gat Asp	aat Asn	684
gca Ala	gga Gly 210	aaa Lys	att Ile	aaa Lys	cca Pro	tcc Ser 215	ttc Phe	aat Asn	ata Ile	gtg Val	cct Pro 220	tta Leu	act Thr	tcc Ser	cgt Arg	732
gtg Val 225	aaa Lys	cct Pro	gat Asp	cct Pro	cca Pro 230	cat His	att Ile	aaa Lys	aac Asn	ctc Leu 235	tcc Ser	ttc Phe	cac His	aat Asn	gat Asp 240	780
gac Asp	cta Leu	tat Tyr	gtg Val	caa Gln 245	tgg Trp	gag Glu	aat Asn	cca Pro	cag Gln 250	aat Asn	ttt Phe	att Ile	agc Ser	aga Arg 255	tgc Cys	828
cta Leu	ttt Phe	tat Tyr	gaa Glu 260	gta Val	gaa Glu	gtc Val	aat Asn	aac Asn 265	agc Ser	caa Gln	act Thr	gag Glu	aca Thr 270	cat His	aat Asn	876
gtt Val	ttc Phe	tac Tyr 275	gtc val	caa Gln	gag Glu	gct Ala	aaa Lys 280	tgt Cys	gag Glu	aat Asn	cca Pro	gaa Glu 285	ttt Phe	gag Glu	aga Arg	924
aat Asn	gtg Val 290	gag Glu	aat Asn	aca Thr	tct Ser	tgt Cys 295	ttc Phe	atg Met	gtc Val	cct Pro	ggt Gly 300	gtt Val	ctt Leu	cct Pro	gat Asp	972
act Thr 305	ttg Leu	aac Asn	aca Thr	gtc Val	aga Arg 310	ata Ile	aga Arg	gtc Val	aaa Lys	aca Thr 315	aat Asn	aag Lys	tta Leu	tgc Cys	tat Tyr 320	1020
gag Glu	gat Asp	gac Asp	aaa Lys	ctc Leu 325	tgg Trp	agt Ser	aat Asn	tgg Trp	agc Ser 330	caa Gln	gaa Glu	atg Met	agt Ser	ata Ile 335	ggt Gly	1068
aag Lys	aag Lys	cgc Arg	aat Asn 340	tcc Ser	aca Thr	ctc Leu	tac Tyr	ata Ile 345	acc Thr	atg Met	tta Leu	ctc Leu	att Ile 350	gtt val	cca Pro	1116
gtc Val	atc Ile	gtc Val 355	gca Ala	ggt Gly	gca Ala	atc Ile	ata Ile 360	gta Val	ctc Leu	ctg Leu	ctt Leu	tac Tyr 365	cta Leu	aaa Lys	agg Arg	1164
ctc Leu	aag Lys 370	att Ile	att Ile	ata Ile	ttc Phe	cct Pro 375	cca Pro	att Ile	cct Pro	gat Asp	cct Pro 380	ggc Gly	aag Lys	att Ile	ttt Phe	1212
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Cont

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Gut

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Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn
260 265 270
Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg
275 280 285
Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp
290 295 300
Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr 305 310 315 320
Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly 325 330 335
Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
340 345 350
Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
355 360 365
Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
370 375 380
Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys 385 390 395 400
Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val
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1 5 10 15
Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser
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Asp Tyr Lys Asp Asp Asp Asp Lys

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·Cht

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15
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Val Gln Pro Pro Val Thr Xaa Leu Ser Val 20 25